

[0144] 2. Plot can be configured by clicking on configure plot and making selections as follows: SNP Assay: Assay of interest can be selected, Plot Type: Select either Cartesian or Polar. Once this is done, the allelic discrimination plot is displayed for the selected SNP assay.

[0145] NOTE: All points in the plot are cyan because all the wells are selected in Plate Layout, by clicking anywhere in the plot or on Plate Layout the wells can be deselected. By doing this the data points in the plot change to the call colors.

[0146] 3. Confirming the control data clusters as expected.

a. Select the wells containing control under the Well Table or Plate Layout to highlight the respective data points in the plot.

b. Check that the data points for each genotype control cluster along the expected axis of the plot.

[0147] 4. In order to confirm only negative control wells are selected click on the cluster at the bottom left corner of the plot and make sure only corresponding wells are selected in the Plate Layout or Well Table.

[0148] It is possible that samples can unexpectedly cluster with the negative controls due to following reasons: samples contain no DNA, samples contain PCR inhibitors and/or samples are homozygous for a sequence deletion.

[0149] 5. In order to review other clusters in the plot, follow the following steps:

[0150] a. Create a box around a cluster by Click-drag a box to select associated wells.

[0151] b. Confirm by checking if corresponding wells are selected in the Plate Layout or Well Table.

[0152] 6. Outliers can be detected if the sample result falls outside the three genotype clusters. In case of outliers detected the results should be confirmed by performing a re-test for outliers as well as the samples that failed to amplify.


[0153] Instructions for Making Manual Calls:

[0154] Manual calls can be performed under the Results tab.

[0155] 1. Select, Allelic Discrimination Plot using the dropdown menu.

[0156] 2. In case the screen doesn't show data analyzed, click on the Analyze option.

[0157] 3. Under the Allelic Discrimination Plot, using the lasso tool samples can be selected for making manual calls.

[0158] 5. Click , button and select the allele call using the apply call dropdown option.

[0159] 6. Click Analyze.

TABLE 12

Cluster Assignment in an allelic discrimination plot	
Content of Samples	Location in AD plot
Allele 1 (homozygous, labeled with VIC dye)	Bottom right corner
Allele 2 (homozygous, labeled with FAM dye)	Top right corner
Alleles 1 and 2 (Heterozygous)	Approximately midway

TABLE 12-continued

Cluster Assignment in an allelic discrimination plot	
Content of Samples	Location in AD plot
No template control	Lower left corner
Undetermined	Anywhere outside the regions described above
No amplification	With NTC cluster in the lower left corner

(TaqMan® SNP Genotyping Assays User Guide (Publication Number MAN0009593 Revision B.0))

1. A method of treating alopecia in a subject in need thereof, the method comprising:

applying to the scalp of the subject a composition containing a phytoestrogen.

2. The method of claim 1, wherein after applying the composition containing a phytoestrogen, the subject subsequently applies a topical minoxidil composition.

3. The method of claim 1, wherein the phytoestrogen is an isoflavone.

4. The method of claim 3, wherein the isoflavone is any one or combination of daidzein, genistein, glycitein, formononetin, biochanin A, daidzin, genistin, glycitin, ononin, sissotrin, acetyldaidzin, acetylgenistin, acetylglycitin, malonyldaidzin, malonylgenistin, malonylglycitin, malonylononin, or malonylsissotrin.

5. A method to determine whether a subject will respond to or benefit from a phytoestrogen based treatment for alopecia, the method comprising:

measuring a variant of SNP rs1013718 in the ESR2 gene of the subject.

6. The method of claim 5, further comprising:

collecting a DNA sample from the subject;

extracting the DNA from the sample;

amplifying DNA segments of the extracted DNA corresponding to a variant of SNP rs1013718 in the ESR2 gene; and

analyzing the data to determine the SNP rs1013718 variant of the subject.

7. The method of claim 5, wherein the variant of SNP rs1013718 is any one or combination of "CC", "CT" or "TT".

8. The method of claim 7, further comprising:

determining that the subject will respond to or benefit from the phytoestrogen based treatment when the variant is "CC".

9. The method of claim 7, further comprising:

determining that the subject has an increased risk of developing female pattern hair loss when the variant is "CC".

10. The method of claim 9, further comprising:

determining that the subject has a lower risk of developing female pattern hair loss when the variant is "CT" or "TT", as compared to the risk of developing female pattern hair loss when the variant is "CC".

11. The method of claim 6, wherein the DNA sample is a saliva sample.

12. The method of claim 6, wherein after extracting the DNA from the sample, the DNA is purified and subsequently quantified.

13. The method of claim 6, wherein the DNA is amplified by a real-time polymerase chain reaction protocol.